



SEQUENCE LISTING

<110> Zankel et al.

<120> MEGALIN-BASED DELIVERY OF THERAPEUTIC COMPOUNDS TO THE BRAIN AND OTHER TISSUES

<130> 31075/40037

<140> 10/812,849

<141> 2004-03-30

<150> US 10/600,862

<151> 2003-06-20

<160> 29

<170> PatentIn version 3.2

<210> 1

<211> 323

<212> PRT

<213> Homo sapiens

<400> 1

Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg Glu Ser
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20 25 30Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His Ala Asp
35 40 45Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu Lys Leu
50 55 60Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile Arg Asn
65 70 75 80Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys Asp Ala
85 90 95Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp Gly Leu
100 105 110Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly
115 120 125Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His
130 135 140

His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser
145 150 155 160

Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser
165 170 175

Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu
180 185 190

Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser
195 200 205

His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile
210 215 220

Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu
225 230 235 240

Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys
245 250 255

His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg
260 265 270

His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu
275 280 285

Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val
290 295 300

Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His
305 310 315 320

Asn Glu Leu

<210> 2
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<212> PRT
<213> Homo sapiens

<400> 2

Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly Lys Phe
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Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His His Lys
20 25 30

Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser Arg Thr

35

40

45

Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser Asp Ile
50 55 60

Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu Lys Leu
65 70 75 80

Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser His Gln
85 90 95

Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile Asp Leu
100 105 110

Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu Glu Ala
115 120 125

Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn
130 135 140

His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg His Ala
145 150 155 160

Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu Lys His
165 170 175

Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val Lys Lys
180 185 190

His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His Asn Glu
195 200 205

Leu

<210> 3
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

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<223> Synthetic primer

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<210> 5
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<212> PRT
<213> Homo sapiens

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Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly Ile Ser
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Val Arg Leu Thr Ser Cys Ala Arg Val Leu His Tyr Lys Glu Lys Ile
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His Glu Tyr Asn Val Leu Leu Asp Thr Leu Ser Arg Ala Glu Glu Gly
35 40 45

Tyr Glu Asn Leu Leu Ser Pro Ser Asp Met Thr His Ile Lys Ser Asp
50 55 60

Thr Leu Ala Ser Lys His Ser Glu Leu Lys Asp Arg Leu Arg Ser Ile
65 70 75 80

Asn Gln Gly Leu Asp Arg Leu Arg Lys Val Ser His Gln Leu Arg Pro
85 90 95

Ala Thr Glu Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala
100 105 110

Gln Ser Ala Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu
115 120 125

Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys
130 135 140

Gln Leu Glu Ile Ser His Gln Lys Leu Lys His Val Glu Ser Ile Gly
145 150 155 160

Asp Pro Glu His Ile Ser Arg Asn Lys Glu Lys Tyr Val Leu Leu Glu
165 170 175

Glu Lys Thr Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp
180 185 190

Leu Ser Ser Arg Val Ser Arg Ala Arg His Asn Glu Leu

195

200

205

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 <212> DNA
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 <220>
 <223> RAP-GAA fusion sequence

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<213> Artificial sequence

<220>
<223> RAP-GAA fusion sequence

<400> 7

Met Arg Gly Pro Ser Gly Ala Leu Trp Leu Leu Leu Ala Leu Arg Thr
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Val Leu Gly Ser Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro
20 25 30

Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu
35 40 45

Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu
50 55 60

Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys
65 70 75 80

Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg
85 90 95

Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly
100 105 110

Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln
115 120 125

Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala
130 135 140

Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg
145 150 155 160

Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu
165 170 175

Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro
180 185 190

Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr
195 200 205

Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu
210 215 220

Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu
225 230 235 240

Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr
245 250 255

Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala
260 265 270

Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His
275 280 285

Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser
290 295 300

Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu
305 310 315 320

Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser
325 330 335

Arg Ala Arg Ala Glu Ala Glu Thr Gly Ala His Pro Gly Arg Pro Arg
340 345 350

Ala Val Pro Thr Gln Cys Asp Val Pro Pro Asn Ser Arg Phe Asp Cys
355 360 365

Ala Pro Asp Lys Ala Ile Thr Gln Glu Gln Cys Glu Ala Arg Gly Cys
370 375 380

Cys Tyr Ile Pro Ala Lys Gln Gly Leu Gln Gly Ala Gln Met Gly Gln
385 390 395 400

Pro Trp Cys Phe Phe Pro Pro Ser Tyr Pro Ser Tyr Lys Leu Glu Asn
405 410 415

Leu Ser Ser Ser Glu Met Gly Tyr Thr Ala Thr Leu Thr Arg Thr Thr
420 425 430

Pro Thr Phe Phe Pro Lys Asp Ile Leu Thr Leu Arg Leu Asp Val Met
435 440 445

Met Glu Thr Glu Asn Arg Leu His Phe Thr Ile Lys Asp Pro Ala Asn
450 455 460

Arg Arg Tyr Glu Val Pro Leu Glu Thr Pro Arg Val His Ser Arg Ala
465 470 475 480

Pro Ser Pro Leu Tyr Ser Val Glu Phe Ser Glu Glu Pro Phe Gly Val
485 490 495

Ile Val His Arg Gln Leu Asp Gly Arg Val Leu Leu Asn Thr Thr Val
500 505 510

Ala Pro Leu Phe Phe Ala Asp Gln Phe Leu Gln Leu Ser Thr Ser Leu
515 520 525

Pro Ser Gln Tyr Ile Thr Gly Leu Ala Glu His Leu Ser Pro Leu Met
530 535 540

Leu Ser Thr Ser Trp Thr Arg Ile Thr Leu Trp Asn Arg Asp Leu Ala
545 550 555 560

Pro Thr Pro Gly Ala Asn Leu Tyr Gly Ser His Pro Phe Tyr Leu Ala
565 570 575

Leu Glu Asp Gly Gly Ser Ala His Gly Val Phe Leu Leu Asn Ser Asn
580 585 590

Ala Met Asp Val Val Leu Gln Pro Ser Pro Ala Leu Ser Trp Arg Ser
595 600 605

Thr Gly Gly Ile Leu Asp Val Tyr Ile Phe Leu Gly Pro Glu Pro Lys
610 615 620

Ser Val Val Gln Gln Tyr Leu Asp Val Val Gly Tyr Pro Phe Met Pro
625 630 635 640

Pro Tyr Trp Gly Leu Gly Phe His Leu Cys Arg Trp Gly Tyr Ser Ser
645 650 655

Thr Ala Ile Thr Arg Gln Val Val Glu Asn Met Thr Arg Ala His Phe
660 665 670

Pro Leu Asp Val Gln Trp Asn Asp Leu Asp Tyr Met Asp Ser Arg Arg
675 680 685

Asp Phe Thr Phe Asn Lys Asp Gly Phe Arg Asp Phe Pro Ala Met Val
690 695 700

Gln Glu Leu His Gln Gly Gly Arg Arg Tyr Met Met Ile Val Asp Pro
705 710 715 720

Ala Ile Ser Ser Ser Gly Pro Ala Gly Ser Tyr Arg Pro Tyr Asp Glu
725 730 735

Gly Leu Arg Arg Gly Val Phe Ile Thr Asn Glu Thr Gly Gln Pro Leu
740 745 750

Ile Gly Lys Val Trp Pro Gly Ser Thr Ala Phe Pro Asp Phe Thr Asn
755 760 765

Pro Thr Ala Leu Ala Trp Trp Glu Asp Met Val Ala Glu Phe His Asp
770 775 780

Gln Val Pro Phe Asp Gly Leu Trp Ile Asp Met Asn Glu Pro Ser Asn
785 790 795 800

Phe Ile Arg Gly Ser Glu Asp Gly Cys Pro Asn Asn Glu Leu Glu Asn
805 810 815

Pro Pro Tyr Val Pro Gly Val Val Gly Gly Thr Leu Gln Ala Ala Thr
820 825 830

Ile Cys Ala Ser Ser His Gln Phe Leu Ser Thr His Tyr Asn Leu His
835 840 845

Asn Leu Tyr Gly Leu Thr Glu Ala Ile Ala Ser His Arg Ala Leu Val
850 855 860

Lys Ala Arg Gly Thr Arg Pro Phe Val Ile Ser Arg Ser Thr Phe Ala
865 870 875 880

Gly His Gly Arg Tyr Ala Gly His Trp Thr Gly Asp Val Trp Ser Ser
885 890 895

Trp Glu Gln Leu Ala Ser Ser Val Pro Glu Ile Leu Gln Phe Asn Leu
900 905 910

Leu Gly Val Pro Leu Val Gly Ala Asp Val Cys Gly Phe Leu Gly Asn
915 920 925

Thr Ser Glu Glu Leu Cys Val Arg Trp Thr Gln Leu Gly Ala Phe Tyr
930 935 940

Pro Phe Met Arg Asn His Asn Ser Leu Leu Ser Leu Pro Gln Glu Pro
945 950 955 960

Tyr Ser Phe Ser Glu Pro Ala Gln Ala Met Arg Lys Ala Leu Thr
965 970 975

Leu Arg Tyr Ala Leu Leu Pro His Leu Tyr Thr Leu Phe His Gln Ala
980 985 990

His Val Ala Gly Glu Thr Val Ala Arg Pro Leu Phe Leu Glu Phe Pro
995 1000 1005

Lys Asp Ser Ser Thr Trp Thr Val Asp His Gln Leu Leu Trp Gly
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Glu Ala Leu Leu Ile Thr Pro Val Leu Gln Ala Gly Lys Ala Glu
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Val Thr Gly Tyr Phe Pro Leu Gly Thr Trp Tyr Asp Leu Gln Thr
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Val Pro Ile Glu Ala Leu Gly Ser Leu Pro Pro Pro Ala Ala
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Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln Trp Val Thr Leu
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Pro Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg Ala Gly Tyr
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Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu Ser Arg
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Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly Glu
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Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu Val
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Leu Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala Arg Asn
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Asn Thr Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly Ala
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Gly Leu Gln Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala
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Pro Gln Gln Val Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr
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Tyr Ser Pro Asp Thr Lys Val Leu Asp Ile Cys Val Ser Leu Leu
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Met Gly Glu Gln Phe Leu Val Ser Trp Cys
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<210> 8
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<212> DNA
<213> Artificial sequence

<220>
<223> RAP-IDU fusion sequence

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<210> 9
 <211> 972
 <212> PRT
 <213> Artificial sequence

<220>

<223> RAP-IDU fusion sequence

<400> 9

Met Arg Gly Pro Ser Gly Ala Leu Trp Leu Leu Leu Ala Leu Arg Thr
1 5 10 15

Val Leu Gly Ser Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro
20 25 30

Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu
35 40 45

Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu
50 55 60

Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys
65 70 75 80

Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg
85 90 95

Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly
100 105 110

Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln
115 120 125

Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala
130 135 140

Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg
145 150 155 160

Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu
165 170 175

Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro
180 185 190

Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr
195 200 205

Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu
210 215 220

Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu
225 230 235 240

Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr
245 250 255

Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala
260 265 270

Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His
275 280 285

Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser
290 295 300

Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu
305 310 315 320

Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser
325 330 335

Arg Ala Arg Ala Glu Ala Glu Thr Gly Glu Ala Pro His Leu Val His
340 345 350

Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser
355 360 365

Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val
370 375 380

Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val Pro
385 390 395 400

His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu Val
405 410 415

Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His
420 425 430

Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly
435 440 445

Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp
450 455 460

Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg
465 470 475 480

Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe
485 490 495

Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser Met
500 505 510

Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly Leu
515 520 525

Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser Phe
530 535 540

His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys
545 550 555 560

His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp
565 570 575

Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu
580 585 590

Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys
595 600 605

Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly
610 615 620

Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met
625 630 635 640

Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr
645 650 655

Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu
660 665 670

Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe
675 680 685

Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro
690 695 700

Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu
705 710 715 720

Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr
725 730 735

Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala
740 745 750

Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His
755 760 765

Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro
770 775 780

Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys
785 790 795 800

Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr
805 810 815

Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala Ala
820 825 830

Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala
835 840 845

Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu
850 855 860

Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln
865 870 875 880

Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys
885 890 895

Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr
900 905 910

Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro
915 920 925

Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp Tyr
930 935 940

Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val
945 950 955 960

Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
965 970

<210> 10
<211> 1398
<212> DNA
<213> Artificial sequence

<220>
<223> RAP-GDNF fusion sequence

<400>	10					
atgggggggtt	cttactcgcg	ggagaagaac	cagcccaagc	cgtccccgaa	acgcgagtcc	60
ggagaggagt	tccgcatttga	gaagtttgaac	cagctgtggg	agaaggccc	gactgcattt	120
cttcctcccg	tgaggctggc	cgagctccac	gctgatctga	agatacagga	gagggacgaa	180
ctcgcttgg	agaaaactaaa	gcttgcacggc	ttggacgaag	atggggagaa	ggaagcgaga	240
ctcatacgca	acctcaatgt	catcttggcc	aagtatggtc	tggacggaaa	gaaggacgct	300
cggcagggtga	ccagcaactc	cctcagtggc	accaggaaag	acgggcttgg	tgacccagg	360
ctggaaaagc	tgtggcacaa	ggcgaagacc	tctggaaat	tctccggcga	agaactggac	420
aagctctggc	gggagttcct	gcatcacaaa	gagaaagttc	acgagtacaa	cgtcctgctg	480
gagaccctga	gcaggaccga	agaaatccac	gagaacgtca	ttagcccttc	ggacctgagc	540
gacatcaagg	gcagcgtcct	gcacagcagg	cacacggagc	tgaaggagaa	gctgcgcagc	600
atcaaccagg	gcctggaccg	cctgcgcagg	gtcagccacc	agggctacag	cactgaggt	660
gagttcgagg	agcccagggt	gattgacctg	ttggacctgg	cgcagtcgc	caacctcact	720
gacaaggagc	tggagggcg	ccgggaggag	ctcaagcact	tcgaagccaa	aatcgagaag	780
cacaaccact	accagaagca	gctggagatt	gcmcacgaga	agctgaggca	cgcagagagc	840
gtgggcgacg	gcgagcgtgt	gagccgcagc	cgcgagaagc	acgcctgct	ggagggcgg	900
accaaggagc	tgggtacac	ggtgaagaag	catctgcagg	acctgtccgg	caggatctcc	960
agagctcggg	ccgaggcaga	aaccggttca	ccagataaac	aaatggcagt	gcttcctaga	1020
agagagcgg	atcggcaggc	tgcagctgcc	aaccagaga	attccagagg	aaaaggtcg	1080
agaggccaga	ggggcaaaaa	ccggggttgt	gtcttaactg	caatacattt	aaatgtcact	1140
gacttgggtc	tgggtatga	aaccaaggag	gaactgattt	ttaggtactg	cagcggctct	1200
tgcgatgcag	ctgagacaac	gtacgacaaa	atattgaaaa	acttatccag	aaatagaagg	1260
tcggtgagt	acaaagttagg	gcaggcatgt	tgcagaccca	tcgccttga	tgtgacctg	1320
tcgttttag	atgataacct	ggtttaccat	attctaagaa	agcattccgc	taaaaggtgt	1380
ggatgtatct	gatctaga					1398

<210> 11
 <211> 463
 <212> PRT
 <213> Artificial sequence

<220>
 <223> RAP-GDNF fusion sequence

<400> 11

Met	Gly	Gly	Ser	Tyr	Ser	Arg	Glu	Lys	Asn	Gln	Pro	Lys	Pro	Ser	Pro
1					5				10				15		

Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu
20 25 30

Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu
35 40 45

Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys
50 55 60

Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg
65 70 75 80

Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly
85 90 95

Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln
100 105 110

Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala
115 120 125

Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg
130 135 140

Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu
145 150 155 160

Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro
165 170 175

Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr
180 185 190

Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu
195 200 205

Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu
210 215 220

Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr
225 230 235 240

Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala
245 250 255

Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His
260 265 270

Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser
275 280 285

Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu
290 295 300

Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser
305 310 315 320

Arg Ala Arg Ala Glu Ala Glu Thr Gly Ser Pro Asp Lys Gln Met Ala
325 330 335

Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro
340 345 350

Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg
355 360 365

Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu
370 375 380

Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser
385 390 395 400

Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser
405 410 415

Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg
420 425 430

Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val
435 440 445

Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
450 455 460

<210> 12
<211> 49
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 12
gcgataggat cctactcgcg ggagaagaac cagcccaagc cgtccccga 49

<210> 13
<211> 57
<212> DNA

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<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 13
gcgataaaacc ggtttctgcc tcggcgcgag ctctggagat cctgccggac aggtcct      57

<210> 14
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 14
gcgataaccg gtgcacacacc cggccgtccc agagcagtg      39

<210> 15
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 15
gcgataactcg agtcaaacacc agctgacgag aaactgc      37

<210> 16
<211> 46
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 16
gcgataaccg gtgagggcccc ccgcacctgg tgcatgtgga cgccgc      46

<210> 17
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 17
gcgataactcg agtcatggat tgcccgaaaa tggggggccct cttgg      45

<210> 18
<211> 33
<212> DNA
<213> Artificial sequence

<220>

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<223> Synthetic primer

<400> 18

acagtgaccgg gttcaccaga taaacaaaatg gca

33

<210> 19

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 19

acagtgcctcg agtctagatc agatacatcc acaccttt

38

<210> 20

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 20

acagtggcca tgggggggttc ttactcgccg gagaagaacc agcccaagcc g

51

<210> 21

<211> 357

<212> PRT

<213> Homo sapiens

<400> 21

Met Ala Pro Arg Arg Val Arg Ser Phe Leu Arg Gly Leu Pro Ala Leu
1 5 10 15

Leu Leu Leu Leu Leu Phe Leu Gly Pro Trp Pro Ala Ala Ser His Gly
20 25 30

Gly Lys Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg
35 40 45

Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu
50 55 60

Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His
65 70 75 80

Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu
85 90 95

Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile
100 105 110

Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys
115 120 125

Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp
130 135 140

Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr
145 150 155 160

Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe
165 170 175

Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr
180 185 190

Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp
195 200 205

Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu
210 215 220

Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg
225 230 235 240

Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg
245 250 255

Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys
260 265 270

Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile
275 280 285

Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys
290 295 300

Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser
305 310 315 320

Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr
325 330 335

Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala
340 345 350

Arg His Asn Glu Leu
355

<210> 22
<211> 378
<212> PRT
<213> Mus musculus

<400> 22

Met Gly Gly Pro Thr Arg Pro Ser Pro Val Ser Leu Leu Ala Leu Gln
1 5 10 15

Arg Lys Met Ala Pro Arg Arg Glu Arg Val Ser Thr Leu Pro Arg Leu
20 25 30

Gln Leu Leu Val Leu Leu Leu Pro Leu Met Leu Val Pro Gln Pro
35 40 45

Ile Ala Gly His Gly Gly Lys Tyr Ser Arg Glu Lys Asn Glu Pro Glu
50 55 60

Met Ala Ala Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu
65 70 75 80

Asn Gln Leu Trp Glu Lys Ala Lys Arg Leu His Leu Ser Pro Val Arg
85 90 95

Leu Ala Glu Leu His Ser Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu
100 105 110

Asn Trp Lys Lys Leu Lys Val Glu Gly Leu Asp Lys Asp Gly Glu Lys
115 120 125

Glu Ala Lys Leu Ile His Asn Leu Asn Val Ile Leu Ala Arg Tyr Gly
130 135 140

Leu Asp Gly Arg Lys Asp Ala Gln Met Val His Ser Asn Ala Leu Asn
145 150 155 160

Glu Asp Thr Gln Asp Glu Leu Gly Asp Pro Arg Leu Glu Lys Leu Trp
165 170 175

His Lys Ala Lys Thr Ser Gly Lys Phe Ser Ser Glu Glu Leu Asp Lys
180 185 190

Leu Trp Arg Glu Phe Leu His Tyr Lys Glu Lys Ile Gln Glu Tyr Asn
195 200 205

Val Leu Leu Asp Thr Leu Ser Arg Ala Glu Glu Gly Tyr Glu Asn Leu
210 215 220

Leu Ser Pro Ser Asp Met Ala His Ile Lys Ser Asp Thr Leu Ile Ser
225 230 235 240

Lys His Ser Glu Leu Lys Asp Arg Leu Arg Ser Ile Asn Gln Gly Leu
245 250 255

Asp Arg Leu Arg Lys Val Ser His Gln Gly Tyr Gly Ser Thr Thr Glu
260 265 270

Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala
275 280 285

Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu Leu Lys His
290 295 300

Phe Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu
305 310 315 320

Ile Ser His Gln Lys Leu Lys His Val Glu Ser Ile Gly Asp Pro Glu
325 330 335

His Ile Ser Arg Asn Lys Glu Lys Tyr Val Leu Leu Glu Glu Lys Thr
340 345 350

Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp Leu Ser Ser
355 360 365

Arg Val Ser Arg Ala Arg His Asn Glu Leu
370 375

<210> 23
<211> 357
<212> PRT
<213> Rat

<400> 23

Leu Arg Asp Arg Val Ser Thr Leu Pro Arg Leu Gln Leu Leu Val Leu
1 5 10 15

Leu Leu Leu Pro Leu Leu Leu Val Pro Gln Pro Ile Ala Gly His Gly
20 25 30

Gly Lys Tyr Ser Arg Glu Lys Asn Glu Pro Glu Met Ala Ala Lys Arg
35 40 45

Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu
50 55 60

Lys Ala Lys Arg Leu His Leu Ser Pro Val Arg Leu Ala Glu Leu His
65 70 75 80

Ser Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Asn Trp Lys Lys Leu
85 90 95

Lys Val Glu Gly Leu Asp Gly Asp Gly Glu Lys Glu Ala Lys Leu Val
100 105 110

His Asn Leu Asn Val Ile Leu Ala Arg Tyr Gly Leu Asp Gly Arg Lys
115 120 125

Asp Thr Gln Thr Val His Ser Asn Ala Leu Asn Glu Asp Thr Gln Asp
130 135 140

Glu Leu Gly Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr
145 150 155 160

Ser Gly Lys Phe Ser Ser Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe
165 170 175

Leu His Tyr Lys Glu Lys Ile His Glu Tyr Asn Val Leu Leu Asp Thr
180 185 190

Leu Ser Arg Ala Glu Glu Gly Tyr Glu Asn Leu Leu Ser Pro Ser Asp
195 200 205

Met Thr His Ile Lys Ser Asp Thr Leu Ala Ser Lys His Ser Glu Leu
210 215 220

Lys Asp Arg Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Lys
225 230 235 240

Val Ser His Gln Gly Tyr Gly Pro Ala Thr Glu Phe Glu Glu Pro Arg
245 250 255

Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Phe Thr Glu Lys
260 265 270

Glu Leu Glu Ser Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile
275 280 285

Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ser His Gln Lys
290 295 300

Leu Lys His Val Glu Ser Ile Gly Asp Pro Glu His Ile Ser Arg Asn
305 310 315 320

Lys Glu Lys Tyr Val Leu Leu Glu Glu Lys Thr Lys Glu Leu Gly Tyr
325 330 335

Lys Val Lys Lys His Leu Gln Asp Leu Ser Ser Arg Val Ser Arg Ala
340 345 350

Arg His Asn Glu Leu
355

<210> 24
<211> 348
<212> PRT
<213> Chicken

<400> 24

Met Gly Ala Thr Arg Thr Leu Val Ala Val Met Ala Ala Phe Leu Ala
1 5 10 15

Val Ser Thr Arg Ala Ser Lys Tyr Thr Arg Glu Ala Asn Glu Gly Leu
20 25 30

Ala Asp Ala Lys Arg Arg Glu Ala Gly Glu Phe Arg Val Val Arg Leu
35 40 45

Asn Gln Val Trp Glu Lys Ala Gln Arg Leu Gln Leu Ser Ala Val Lys
50 55 60

Leu Ala Glu Leu His Ser Asp Leu Lys Ile Gln Glu Lys Asp Glu Leu
65 70 75 80

Ser Trp Lys Lys Leu Lys Ala Glu Gly Leu Gly Glu Asp Gly Glu Lys
85 90 95

Glu Ala Lys Leu Arg Arg Asn Ile Asn Val Ile Met Thr Lys Tyr Gly
100 105 110

Met Asn Gly Lys Lys Asp Ser His Leu Thr Asp Thr Asn Tyr Ile Lys
115 120 125

Asp Gly Thr Glu Ser Asp Thr Leu Asp Asp Pro Arg Leu Glu Lys Leu
130 135 140

Trp Ser Lys Ala Lys Thr Ser Gly Lys Phe Ser Asp Glu Glu Leu Asp
145 150 155 160

Lys Leu Trp Arg Glu Phe Lys His His Lys Glu Lys Ile Arg Glu Tyr
165 170 175

Asn Ile Leu Leu Glu Thr Val Ser Arg Thr Glu Asp Ile His Lys Lys
180 185 190

Val Ile Asn Pro Ser Glu Glu Asn Pro Val Lys Glu Glu Val Leu His
195 200 205

Asn Lys His Arg Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly
210 215 220

Phe Glu Arg Leu Arg Lys Val Ser His Gln Gly Tyr Asp Ala Thr Ser
225 230 235 240

Glu Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Met Ala Lys Ser
245 250 255

Ala Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu Leu Lys
260 265 270

His Phe Glu Ala Lys Ile Glu Lys His His His Tyr Gln Lys Gln Leu
275 280 285

Glu Ile Ser His Glu Lys Leu Lys His Ile Glu Gly Thr Gly Asp Lys
290 295 300

Glu His Leu Asn Arg Asn Arg Glu Lys Tyr Ala Met Leu Glu Glu Lys
305 310 315 320

Thr Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp Leu Ser
325 330 335

Ser Arg Ile Ser Gln Gly Leu Gln His Asn Glu Leu
340 345

<210> 25
<211> 331
<212> PRT
<213> Zebrafish

<400> 25

Met Ala Gly Lys Tyr Ser Lys Glu Met Asn Glu Lys Asn Ala Ser Asp
1 5 10 15

Lys Ser Asn Asn Gln Val Glu Phe Arg Ile Ala Lys Leu Asn Gln Val
20 25 30

Trp Glu Lys Ala Ile Arg Met Gln Leu Ala Pro Val Arg Leu Ser Glu
35 40 45

Leu His Ser Asp Leu Lys Ile Gln Glu Lys Asp Glu Leu Gln Trp Lys
50 55 60

Lys Leu Lys Ala Glu Gly Met Asp Glu Asp Gly Glu Arg Glu Ala Lys
65 70 75 80

Leu Arg Arg Asn Phe Asn Ile Ile Leu Ala Lys Tyr Gly Met Asp Gly
85 90 95

Lys Lys Asp Thr Arg Thr Leu Asp Ser Asn Arg Leu Lys Asp His Glu
100 105 110

Val Lys Ile Gly Asp Thr Phe Asp Asp Pro Lys Leu Asp Lys Leu Trp
115 120 125

Asn Lys Ala Arg Thr Ser Gly Lys Phe Ser Asp Glu Glu Leu Gln Thr
130 135 140

Leu His Arg Glu Phe Gln His His Lys Asp Lys Ile His Glu Tyr Asn
145 150 155 160

Ile Val Met Asp Thr Val Ser Arg Thr Glu Glu Ile His Lys Asn Val
165 170 175

Ile Ser Pro Leu Glu Gly Asp Val Lys Glu Asn Val Leu His Gln Lys
180 185 190

His Thr Asp Leu Lys Gln Arg Met Arg Asp Leu Asn Gln Gly Phe Glu
195 200 205

Arg Leu Arg Lys Ile Thr His Glu Gly Tyr Thr Asp Asp Ser Glu Phe
210 215 220

Arg Glu Pro Arg Val Ile Glu Leu Trp Glu Met Ala Lys Arg Ser Asn
225 230 235 240

Leu Ser Glu Asp Glu Leu Asp Ser Leu Lys Glu Glu Leu Arg His Phe
245 250 255

Glu Thr Lys Val Glu Lys His Gln His Tyr Gln Glu Gln Leu Glu Leu
260 265 270

Ser His Gln Lys Leu Lys His Val Glu Ala Leu Gly Asp Glu Asp His
275 280 285

Ile Met Arg Asn Lys Glu Lys Tyr Asn Thr Leu Ala Glu Lys Ala Arg
290 295 300

Glu	Met	Gly	Tyr	Lys	Met	Lys	Lys	His	Leu	Gln	Asp	Leu	Thr	Asn	Lys
305					310					315					320
Leu	Ser	Lys	Asn	Gly	Leu	Gln	His	Asn	Glu	Leu					
					325				330						
<210>	26														
<211>	379														
<212>	PRT														
<213>	Fruit fly														
<400>	26														
Met	Val	Arg	Ser	Ala	Leu	Val	Val	Ala	Ala	Ile	Ala	Leu	Ser	Val	Leu
1					5				10					15	
Ile	Ala	Leu	Gln	Gly	Val	Asp	Ala	Asp	Lys	Lys	Gln	Ser	Lys	Lys	Tyr
					20				25					30	
Ser	Lys	Glu	Ala	Asn	Asp	Pro	His	Phe	Gln	Gln	Val	Lys	Gln	Glu	Lys
					35			40					45		
Tyr	Asp	Pro	Asp	Phe	Lys	Ser	Ile	Gln	Arg	Pro	Phe	Arg	Met	Ala	Lys
					50			55					60		
Leu	Asn	Leu	Val	Trp	Ala	Lys	Ala	Gln	Asn	Arg	Leu	Thr	Glu	Pro	Lys
						65			70			75			80
Leu	Lys	Ser	Leu	Tyr	Met	Glu	Leu	Lys	Ile	His	Asp	Lys	Glu	Glu	Ile
						85			90					95	
Ala	Trp	Lys	Gln	Leu	Asn	Ser	Gln	His	Lys	Asp	Lys	Asp	Gly	Leu	Lys
						100			105					110	
Ala	Asp	Glu	Leu	Arg	Arg	Lys	Leu	Ile	Gly	Ile	Met	Ser	Ser	Tyr	Asp
						115			120					125	
Leu	Leu	Glu	His	Phe	Asp	Asp	Thr	Gln	Asp	Thr	Glu	Lys	Leu	Lys	Pro
						130			135					140	
Tyr	Lys	Lys	Phe	His	Asp	Ala	Glu	Glu	Arg	His	Arg	Asn	Lys	Ser	Leu
						145			150			155			160
Phe	Lys	Asp	Lys	Lys	Leu	Asn	Arg	Leu	Trp	Glu	Lys	Ala	Glu	Ile	Ser
						165				170			175		
Gly	Phe	Thr	Ala	Glu	Glu	Leu	Lys	Ser	Leu	Lys	Gln	Glu	Phe	Asp	His
						180				185			190		

His Gln Asp Lys Val Asp Val Tyr Tyr Ser Leu Leu Glu Asn Ile Gly
195 200 205

Thr Val Asp Thr Asp Lys His Glu Asn Ala Ile Asn Thr Glu Asp Leu
210 215 220

Asp Thr Tyr Asn Leu Ile Ser Asn Asp Val Asn Glu Asn Asp Ile Lys
225 230 235 240

Thr His Ala Gln Asn Val Lys Ser Phe Glu Asn Asp Leu Asn Thr Leu
245 250 255

Arg Gly His His Thr Gly Ile Lys Asp His Tyr Asp Arg Leu Glu Arg
260 265 270

Leu Val Ser Ser Gly Pro His Ser Gln Asp Phe Ile Glu Pro Lys Val
275 280 285

Gln Gly Leu Trp Arg Val Ala Gln Ala Ser Asn Phe Thr Val Lys Glu
290 295 300

Leu Glu Ser Ile Lys Thr Glu Leu His His Phe Glu Ser Arg Leu Leu
305 310 315 320

Lys Leu Arg His Leu His Ala Glu His Ala Leu Gln Lys Glu Lys Tyr
325 330 335

Lys Gly Glu Lys Val Lys Asp Lys Ser Ser Arg Phe Glu Glu Met Glu
340 345 350

Asp Gln Leu Lys Lys Gln Thr Arg Lys Val Glu Lys Leu Gln Glu Asn
355 360 365

Ile Glu Lys Thr Ile Phe Lys His Thr Glu Leu
370 375

<210> 27
<211> 400
<212> PRT
<213> Mosquito

<400> 27

Glu Leu Cys Pro Ile Ala Arg Arg Lys Arg Gly Ile Lys His Thr Leu
1 5 10 15

Thr Met Pro Leu Phe Thr Arg Leu Cys Val Ile Val Phe Thr Val Leu
20 25 30

Val Cys Asn His Val Val Gln Ser Glu Lys Ala His Ser Lys Tyr Ser
35 40 45

Lys His Ala Asn Ala Leu Pro Asp Ser Glu Ile Tyr Glu Pro Asp Phe
50 55 60

Arg Asn Ile Gln Arg Pro Phe Arg Met Ala Lys Leu Asn Leu Val Trp
65 70 75 80

Thr Lys Ala Gln His Arg Leu Thr Glu Pro Lys Leu Lys Ser Leu Tyr
85 90 95

Thr Glu Leu Lys Leu His Asp Lys Glu Glu Leu Thr Tyr Lys Gln Leu
100 105 110

Lys Glu Lys Asp Lys Asp Gly Leu Lys Glu Ala Glu Leu Arg Asn Lys
115 120 125

Leu Val Ser Ile Met Ser Thr Tyr Gly Leu Leu Glu His Phe Asp Asp
130 135 140

Thr Gln Asp Pro Glu Lys Tyr Lys Leu Ala Lys Ser Ser Asp Gly Ala
145 150 155 160

Pro Lys Lys Asp Thr Tyr Lys Asn Lys Ser Leu Phe Lys Asp Lys Lys
165 170 175

Leu Asn Lys Leu Trp Asp Lys Ala Glu Ser Ala Gly Phe Thr Lys Glu
180 185 190

Glu Leu Asp Ala Leu Arg Glu Glu Phe Asp His His Gln Ala Lys Ile
195 200 205

Asp Val Tyr Tyr Ser Leu Leu Glu Arg Leu Gly Asp Asp Asp Asp Gly
210 215 220

Gly Ala Ala Gly Gln Gly Ser Arg Arg Asp Asp Asp Ala Leu Leu Asn
225 230 235 240

Ala Val Asn Asp Glu Glu His Asp Arg Tyr Asn Glu Val Asp Arg Ala
245 250 255

Glu Glu Thr Asp Arg Ser Gln Pro Gly Ala Asn Lys Gln His Ala Tyr
260 265 270

Leu His Lys Ser Asn Gln Leu Arg Glu Lys His Arg Glu Ile Arg Asp
275 280 285

Asn Phe Asp Arg Leu Asp Arg Ile Ala Ser Lys Gly Pro Lys Ser Gln
290 295 300

Asp Phe Val Glu Pro Lys Val Gln Gly Leu Trp Arg Val Ala Leu Ala
305 310 315 320

Ser Asp Phe Ser Ala Asp Glu Leu Ala Ser Leu Lys Val Glu Leu Leu
325 330 335

His Tyr Glu Ser Arg Leu Leu Lys Leu Arg His Met His Ala Glu His
340 345 350

Ala Leu Ser Leu Glu Lys His Lys His Ser Asp Ala Lys Ala Asp Thr
355 360 365

His Lys Leu Met Glu Asp Asn Ile Lys Lys Gln Thr Arg Lys Val Glu
370 375 380

Lys Met Gln Glu Glu Val Glu Arg Arg Ile Phe Lys His Ser Glu Leu
385 390 395 400

<210> 28
<211> 331
<212> PRT
<213> Flatworm

<400> 28

Met Arg Asn His Phe Ser Phe Leu Leu Phe Leu Leu Val Ile Gly Ser
1 5 10 15

Ala His Asn Lys Lys Thr Gln Tyr Arg Thr Glu Arg Ile Asn Phe Ile
20 25 30

Tyr Glu Lys Ala Leu Gln His Val Thr Asp Arg Gln Asn Leu Ala Arg
35 40 45

Leu Glu Lys Glu Leu Ser Gly Tyr Asp Ala Ile Tyr Leu Ala Ser Lys
50 55 60

Ser Asn Arg Gln Gly Thr Gln Gly Thr Lys Glu Ile Asp Lys Ile Asp
65 70 75 80

Asp Lys Leu Gly Lys Ile Leu Glu Lys Tyr Gly Leu Glu Lys Ala Val
85 90 95

Leu Ala Phe Lys Glu Lys Tyr Lys His Lys Asn Leu Phe Gln Gln Thr
100 105 110

Asp Asp Asn Glu Pro Leu Pro Ser Gly Lys Phe Thr Asp Gln Asn Leu
115 120 125

Gln Lys Leu Trp Ser Gln Ala Gln Asn Gly Lys Phe Ser Gln Lys Glu
130 135 140

Leu Asn Ala Leu His Gly Glu Leu Lys Glu Val Glu Gln Lys Met Arg
145 150 155 160

Val Tyr Glu Asp Gln Leu Asp Asp Phe Lys Lys Val Pro His Glu Asn
165 170 175

Ser Ile Gln His Asp Ile Glu Ser Ile Gly Asp Lys Thr Lys Lys Leu
180 185 190

Lys Ala Ala Asn Arg Glu Leu Asn Asp His Leu Asp Glu Val His Arg
195 200 205

Lys Val Thr Ser Glu Glu Phe Ser Pro Phe Asn Glu Pro Arg Val Lys
210 215 220

Arg Leu Trp Lys Leu Ala Gln Glu Asn Glu Lys Leu Thr Pro His Glu
225 230 235 240

Leu Ser Val Leu Lys Asp Glu Leu Ser His Phe Glu Ser Gln Leu Lys
245 250 255

Lys Ile Glu Phe His Lys Val Phe Phe Phe Val Ala Asn Ser Cys Pro
260 265 270

Lys Arg Gly Lys Asn Glu Glu Val Ser Arg Leu Gln Glu Asp Ala Glu
275 280 285

Glu Arg Gly Lys Asp Lys Ser Gln Val Tyr Glu Asn Leu Glu Leu Ser
290 295 300

Ile Lys His Glu Lys Leu Asn Arg Lys Ala Arg Lys Leu Glu Lys Tyr
305 310 315 320

Ile Glu Glu Lys Ile Ile His Arg Glu Leu
325 330

<210> 29
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 29

Ala Glu Ala Glu Thr Gly
1 5